Amendments to the Specification:

Please replace the paragraph starting at page 58, line 27, through page 58, line 10, with the following paragraph:

-- The generated EST sequences are searched against available databases, including the "nt", "nr", "est", "gss" and "htg" databases available through NCBI to determine putative identities for ESTs matching to known genes or other ESTs. Relative EST frequency level can then be calculated using known methods. Functional characterization of ESTs with known gene matches are made according to any known method. Preferably, generated EST sequences are compared to the non-redundant Genbank/EMBL/DDBJ and dbEST databases using the BLAST algorithm (8). A minimum value of $P = 10^{-10}$ and nucleotide sequence identity >95%, where the sequence identity is non-contiguous or scattered, are required for assignments of putative identities for ESTs matching to known genes or to other ESTs. Construction of a non-redundant list of genes represented in the EST set is done with the help of Unigene, Entrez and PubMed at the National Center for Biotechnology Information (NCBI) site ~~(http://www.ncbi.nlm.nih.gov/)~~. Relative gene expression frequency is calculated by dividing the number of EST copies for each gene by the total number of ESTs analyzed.--

Please replace the paragraph starting at page 93, lines 10-17, with the following paragraph:

--Sequences were manually edited or edited using Sequencher software (GeneCodes). All edited EST sequences were compared to the non-redundant Genbank/EMBL/DDBJ and dbEST databases using the BLAST algorithm (8). A minimum value of $P = 10^{-10}$ and nucleotide sequence identity >95% were required for assignments of putative identities for ESTs matching to known genes or to other ESTs. Construction of a non-redundant list of genes represented in the EST set was done with the help of Unigene, Entrez and PubMed at the National Center for Biotechnology Information (NCBI) site ~~(Web address: www.ncbi.nlm.nih.gov/)~~.--

Please replace the paragraph starting at page 97, lines 10-17, with the following paragraph:

--Sample RNA from either normal, mild or severe OA cartilage was labelled with fluorescent dye Cy3 or Cy5, and Universal Human Reference RNA (Stratagene, Product#

740000) labelled with the remaining fluorescent dye and normalized intensities for each sample RNA determined having taken into account intensity differences as a result of the use of the different dyes. Analysis was performed using GeneSpring 4.1.5 and genes demonstrating a stage specific difference in expression intensity of greater than 2 fold when compared to either the intensity ~~form~~ from the normal cartilage or any other stage specific cartilage RNA were identified.--